



Bacterial Whole Genome Sequencing Report

October 13, 2023

Sample ID: SRR26282520

Sequencing Technology

Nextera XT DNA Library Preparation
MiSeq 2 x 250 Read Generation

Sequence Statistics		Quality Scale	
		Low	High
Filename	SRR26282520-R1.fastq.gz		SRR26282520-R2.fastq.gz
File size	80.0 MB		95.6 MB
Mean Read Score	37.07		34.98
Q30 Passing	96.9%		86.9%
Sequence Depth	52.7X	Calculated by number of reads x 240/Genome Length	
Genome Length	5,000,000bp	Based on MLST identification	

Assembly Statistics				Quality Scale		
				Low	High	
Scaffolds	Total length	Longest scaffold	Scaffolds >1K nt	Genome >1K nt	N50	L50
840	4,869,513	97,063	368	97.05	25,688	56

De novo assembly performed using SPAdes v3.13.0 .

Multi Locus Sequence Typing (MLST)

Organism ID: **Escherichia coli** Schema-Sequence type: **ecoli_achtman_4-152**

MLST Detail: adk(11) fumC(63) gyrB(7) icd(1) mdh(14) purA(7) recA(7)

Data obtained using 2.23.0. Software website: <https://github.com/tseemann/mlst>

Information on MLST schemes and allelic profiles can be found at pubMLST.org

Antimicrobial Resistance Analysis

Results were obtained using [AMRFinder](#). AMRFinder uses BLASTX to search a hierarchy of gene families with predetermined cutoffs.

AMRFinder

Contig id	Start	Stop	Gene symbol	Sequence name	Scope	Element Subtype	% Coverage of reference sequence	% Identity to reference sequence	Class	Subclass
NODE_163_length_8506_cov_333.220193	34	834	aph(3'')-Ib	aminoglycoside O-phosphotransferase APH(3'')-Ib	core	AMR	100.0	100.0	AMINOGLYCOSIDE	STREPTOMYCIN
NODE_163_length_8506_cov_333.220193	837	1670	aph(6)-Id	aminoglycoside O-phosphotransferase APH(6)-Id	core	AMR	100.0	100.0	AMINOGLYCOSIDE	STREPTOMYCIN
NODE_163_length_8506_cov_333.220193	3009	4205	tet(A)	tetracycline efflux MFS transporter Tet(A)	core	AMR	100.0	100.0	TETRACYCLINE	TETRACYCLINE
NODE_163_length_8506_cov_333.220193	7537	8349	sul2	sulfonamide-resistant dihydropteroate synthase Sul2	core	AMR	100.0	100.0	SULFONAMIDE	SULFONAMIDE
NODE_309_length_1785_cov_1547.853438	351	992	qnrB19	quinolone resistance pentapeptide repeat protein QnrB19	core	AMR	100.0	100.0	QUINOLONE	QUINOLONE
NODE_39_length_33698_cov_11.694379	29376	30161	aadA1	ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA1	core	AMR	100.0	100.0	AMINOGLYCOSIDE	STREPTOMYCIN
NODE_39_length_33698_cov_11.694379	30222	30743	sat2	streptothricin N-acetyltransferase Sat2	core	AMR	100.0	100.0	STREPTOTHRICIN	STREPTOTHRICIN
NODE_39_length_33698_cov_11.694379	30841	31311	dfrA1	trimethoprim-resistant dihydrofolate reductase DfrA1	core	AMR	100.0	100.0	TRIMETHOPRIM	TRIMETHOPRIM
NODE_40_length_33396_cov_18.728155	1954	3309	glpT_E448K	Escherichia fosfomycin resistant GlpT	core	POINT	100.0	99.78	FOSFOMYCIN	FOSFOMYCIN

AMRFinder

Revision 3.11.2

<https://github.com/ncbi/amr/wiki>

Definitions were taken from the AMRFinder documentation.

Target Identifier- This is from the FASTA define for the DNA sequence

Contig id- Contig name

Start- 1-based coordinate of first nucleotide coding from protein in DNA sequence on contig

Stop- 1-based coordinate of last nucleotide coding for protein in DNA sequence on contig

Gene symbol- Gene or gene-family symbol for protein hit

Protein name- Full-text name for the protein

Method- Type of hit found by AMRFinder one of five options

ALLELE- 100% sequence match over 100% of length to a protein named at the allele level in the AMRFinder database

EXACT- 100% sequence match over 100% of length to a protein in the database that is not a named allele

BLAST- BLAST alignment is >90% of length and >90% identity to a protein in a the AMRFinder database

PARTIAL- BLAST alignment is >50% of length, but <90% of length and >90% identity

HMM- HMM was hit above the cutoff, but there was not a BLAST hit that met standards for BLAST or PARTIAL

Target length- The length of the query protein. The length of the BLAST hit for translated-DNA searches

Reference protein length- The length of the AMR Protein in the database (NA if HMM-only hit)

Scope- The AMRFinderPlus database is split into core AMR proteins that are expected to have an effect on resistance and plus proteins of interest added with less stringent inclusion criteria. These may or may not be expected to have an effect on phenotype

Element subtype- Further elaboration of functional category into *ANTIGEN*, *BIOCIDE*, *HEAT*, *METAL*, *PORIN* if more specific category is available, otherwise the element is repeated

% Coverage of reference protein- % covered by blast hit (NA if HMM-only hit)

% Identity to reference protein- % amino-acid identity to reference protein (NA if HMM-only hit)

Alignment length- Length of BLAST alignment in amino acids (NA if HMM-only hit)

Accession of closest protein- RefSeq accession for protein hit by BLAST (NA if HMM-only hit)

Name of closest protein- Full name assigned to the AMRFinder database protein (NA if HMM-only hit)

HMM id- Accession for the HMM

HMM description- The family name associated with the HMM